

WEST Search History

DATE: Monday, April 18, 2005

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
	<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L17	L16 and serogroup B	42
<input type="checkbox"/>	L16	L15 and meningitidis	249
<input type="checkbox"/>	L15	L14 and CpG	318
<input type="checkbox"/>	L14	neisseria and adjuvant	2626
<input type="checkbox"/>	L13	L12 and adjuvant	2626
<input type="checkbox"/>	L12	L11 and (CpG or adjuvant)	2714
<input type="checkbox"/>	L11	L10 and (CpG or adjuvant or DNA adjuvant or immunostimulatory nucleic acid)	2714
<input type="checkbox"/>	L10	neisseria	6972
<input type="checkbox"/>	L9	L8 and (adjuvant or CpG or DNA adjuvant)	15
<input type="checkbox"/>	L8	L7 and neisseria	39
<input type="checkbox"/>	L7	l2 or l3 or l4 or l5 or l6	231
<input type="checkbox"/>	L6	pizza-m.in.	32
<input type="checkbox"/>	L5	pizza-mariagrazia.in.	40
<input type="checkbox"/>	L4	giuliani-marzia-m.in.	7
<input type="checkbox"/>	L3	rappuoli-rino.in.	92
<input type="checkbox"/>	L2	grandi-guido.in.	104
<input type="checkbox"/>	L1	grangi-guido.in.	0

END OF SEARCH HISTORY

BEST AVAILABLE COPY

150873

Shears, Beverly

From: Chan, Christina
Sent: Monday, April 18, 2005 8:55 AM
To: Chan, Christina; Minnifield, Nita; STIC-Biotech/ChemLib
Cc: Shears, Beverly
Subject: RE: rush sequence search

This rush is for Beverly.

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Chan, Christina
Sent: Monday, April 18, 2005 8:54 AM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush sequence search

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita
Sent: Sunday, April 17, 2005 9:00 AM
To: Chan, Christina
Subject: rush sequence search

Christina, please approve, 2 month amdt.

STIC

09/914454

Please do an commercial and interference sequence search
on SEQ ID NO: 31 of the above application.

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OM protein - protein search, using sw model

Run on: April 18, 2005, 10:16:59 ; Search time 44 Seconds
(without alignments)

748.187 Million cell updates/sec

Title: US-09-914-454b-31

Sequence: 1 MKXYLFRAALYGLAAILAA.....KTTGYWQLPENGKPEYRP 441

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA.*

1: /cgn2_6/ptodate/1/1aa/5A.COMB.pep.*
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3: /cgn2_6/ptodate/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodate/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodate/1/1aa/PCUS.COMB.pep.*
6: /cgn2_6/ptodate/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605.5	25.9	396	US-09-252-991A-19425	Sequence 19425, A
2	314.5	13.4	367	US-09-488-039A-10054	Sequence 10054, A
3	275	11.8	365	US-09-543-681A-6366	Sequence 6366, Ap
4	112	4.8	577	US-09-252-991A-25632	Sequence 25632, A
5	110.5	4.7	342	US-09-270-767-45316	Sequence 45316, A
6	102.5	4.4	1190	US-09-252-991A-21474	Sequence 21474, A
7	100	4.3	3562	US-09-679-279-14	Sequence 14, Appl
8	98.5	4.2	543	US-09-902-540-15614	Sequence 15614, A
9	98.5	4.2	986	US-08-311-731A-2	Sequence 2, Appl
10	98	4.2	1053	US-09-252-991A-24665	Sequence 24665, A
11	98	4.2	3567	US-07-642-734C-4	Sequence 4, Appl
12	98	4.2	3567	US-08-439-009A-4	Sequence 4, Appl
13	97.5	4.2	457	US-09-252-991A-30850	Sequence 30850, A
14	96.5	4.1	1118	US-09-252-991A-32439	Sequence 32439, A
15	96.5	4.1	1118	US-09-252-991A-32439	Sequence 32439, A
16	95.5	4.1	1803	US-08-487-183A-12	Sequence 12, Appl
17	95	4.1	1411	US-09-902-540-15978	Sequence 15978, A
18	94.5	4.0	548	US-09-252-991A-23628	Sequence 23628, A
19	94.5	4.0	548	US-07-903-047-8	Sequence 8, Appl
20	94.5	4.0	548	US-08-460-934-2	Sequence 2, Appl
21	94.5	4.0	548	US-08-783-118-2	Sequence 2, Appl
22	94.5	4.0	548	US-09-111-752-14	Sequence 14, Appl
23	94.5	4.0	548	US-09-380-061B-16	Sequence 16, Appl
24	94.5	4.0	548	US-08-487-183A-14	Sequence 14, Appl
25	94.5	4.0	548	US-09-396-154-28	Sequence 28, Appl
26	94.5	4.0	548	US-09-581-241A-4	Sequence 4, Appl
27	94.5	4.0	548	US-09-581-241A-6	Sequence 6, Appl
				US-09-581-241A-8	Sequence 8, Appl

28	94.5	4.0	568	US-08-460-934-6	Sequence 6, Appl
29	94.5	4.0	568	US-08-782-118-6	Sequence 6, Appl
30	94.5	4.0	636	US-08-460-934-9	Sequence 9, Appl
31	94.5	4.0	636	US-08-782-118-9	Sequence 9, Appl
32	94.5	4.0	1369	US-09-711-164-312	Sequence 312, Appl
33	94	4.0	503	US-09-134-001C-4214	Sequence 4214, Ap
34	94	4.0	503	US-09-710-279-1810	Sequence 1810, Ap
35	93.5	4.0	548	US-09-602-628-10	Sequence 10, Appl
36	93.5	4.0	561	US-09-252-991A-20870	Sequence 20870, A
37	93.5	4.0	561	US-09-477-135A-129	Sequence 129, App
38	93	4.0	547	US-09-252-991A-27743	Sequence 27743, A
39	93	4.0	5087	US-09-144-085-1	Sequence 1, Appl
40	92.5	4.0	548	US-07-675-211-2	Sequence 2, Appl
41	92.5	4.0	548	US-07-603-047-2	Sequence 2, Appl
42	92.5	4.0	548	US-08-076-042-2	Sequence 2, Appl
43	92.5	4.0	548	US-09-380-061B-14	Sequence 14, Appl
44	92.5	4.0	548	US-09-396-154-27	Sequence 27, Appl
45	91.5	3.9	683	US-09-252-991A-33038	Sequence 33038, A

ALIGNMENTS

RESULT 1	US-09-252-991A-19425	Application US/09252991A
Sequence 19425, A	Patent No. 6551795	GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.	TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS	FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18	PRIOR FILING DATE: 1998-02-18	PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18	PRIOR APPLICATION NUMBER: US 60/094,190	PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142	SEQ ID NO 19425	LENGTH: 396
TYPE: PRT	ORGANISM: Pseudomonas aeruginosa	US-09-252-991A-19425
Query Match	25.9%; Score 605.5; DB 4; Length 396;	Best Local Similarity 33.7%; Pred. No. 7.2e-55;
Matches 143; Conservative 60; Mismatches 154; Indels 67; Gaps 10;		
15 AAILAACOSKSIQTFFQPDTSVINGPDRPVGIPDPAGTIVGGGAVYTVPHLSLPHMAA 74		
30 AALLTNC-----DCKEPP--PKRPLV-----TNSVPMALRATSD 66		
75 QDFAKLSGFRUGCANLKNRQGMQVCAQAFQTPVHSFOAKOFFEYFTPMQV--AGNGS 132		
67 ADLAFNMRASACARLADPVMGECASATVAADPTAVRAFLQRMQVYSLSRSSNGD 126		
133 LAGTVGYEPLKGDRTTAQAPRIVIGTIPDDFISVPLPAGIRSKALVRIRQTKNSG 192		
127 -QGLTGYEPLVHSGESKTPVGVVDDLVVALES-----VPELKKR-- 175		
193 TIDNTGTTAALSRPITARTTAIKRGREGSRFLPYHTRNOI--NGCALDGKAPILGYA 250		
176 -----LRGRLEGVLRKYDDAATIRONGSS-----APVLAWL 207		
251 EDPVELFPHNIGSGRLKTPSGKTRIGYADKXHEPPIYSIGRYMADKYLKLGQTSMOGI 310		
208 GDFMDQFQIQSGSGRIQLEDRORLRIGYDNGHPYKVGWLVLEQGLVPEKESIMKRI 267		
311 KSYMRNPORLAEVLGONPSYIFPRLAGSSNDGVPALGTPLMGVEYAGAVDRHYTTLGA 370		
268 RMAEKNPVRVSELASNPSPVFF--SLRPDSDESRGSLNVLTLTGYSVAIDRKVIPLGS 326		

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OK protein - protein search, using sw model

Run on: April 18, 2005, 09:56:39 ; Search time 173 Seconds
(without alignments)
985,904 Million cell updates/sec

Title: US-09-914-454B-31

Perfect score: 2340

Sequence: 1 MKXYLFRALYGYIAAIIAA.....KTGYVWQLPNCKPEYRP 441

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2340	100.0	441	4 AAB23783	Aab23783 Neisseria
2	2333	99.7	441	3 AAY75911	Aay75911 Neisseria
3	2333	99.7	441	3 AAY75920	Aay75920 Neisseria
4	2333	99.7	441	3 AAY75927	Aay75927 Neisseria
5	2333	99.7	441	3 AAY75910	Aay75910 Neisseria
6	2333	99.7	441	3 AAY75915	Aay75915 Neisseria
7	2333	99.7	441	3 AAY75909	Aay75909 Neisseria
8	2333	99.7	441	3 AAY75659	Aay75659 Neisseria
9	2333	99.7	441	3 AAY75910	Aay75910 Neisseria
10	2333	99.7	441	3 AAY75929	Aay75929 Neisseria
11	2333	99.7	441	3 AAB25636	Aab25636 N. mening
12	2333	99.7	441	3 AAB25635	Aab25635 N. mening
13	2333	99.7	441	3 AAB58565	Aab58565 N. mening
14	2333	99.7	441	3 AAB58566	Aab58566 N. mening
15	2330	99.6	441	3 AAY75914	Aay75914 Neisseria
16	2330	99.6	441	3 AAY75926	Aay75926 Neisseria
17	2330	99.6	441	3 AAY75916	Aay75916 Neisseria
18	2330	99.6	441	3 AAY75941	Aay75941 Neisseria
19	2330	99.6	441	4 AAB84747	Aab84747 Amino acil
20	2330	99.6	441	4 AAY75925	Aay75925 Neisseria
21	2326	99.4	441	3 AAY75913	Aay75913 Neisseria
22	2325	99.3	441	3 AAY75921	Aay75921 Neisseria
23	2324	99.3	441	3 AAY75913	Aay75913 Neisseria
24	2321	99.2	441	3 AAY75928	Aay75928 Neisseria
25	2318	99.1	441	3 AAY75934	Aay75934 Neisseria

26	2317	99.0	441	3 AAY75936	Aay75936 Neisseria
27	2307	98.6	441	3 AAY75923	Aay75923 Neisseria
28	2307	98.6	441	3 AAY75937	Aay75937 Neisseria
29	2302	98.4	441	3 AAY75660	Aay75660 Neisseria
30	2302	98.4	441	3 AAY75792	Aay75792 Neisseria
31	2302	98.4	441	3 AAY75930	Aay75930 Neisseria
32	2302	98.4	441	3 AAB25638	Aab25638 N. mening
33	2302	98.4	441	3 AAB58568	Aab58568 N. mening
34	2302	98.4	441	6 AAB23697	Aab23697 Genome de
35	2297	98.2	441	3 AAY75919	Aay75919 Neisseria
36	2297	98.2	441	3 AAY75931	Aay75931 Neisseria
37	2297	98.2	441	3 AAY75924	Aay75924 Neisseria
38	2295	98.1	441	3 AAY75918	Aay75918 Neisseria
39	2295	98.1	441	3 AAY75917	Aay75917 Neisseria
40	2295	98.1	441	3 AAY75932	Aay75932 Neisseria
41	2295	98.1	441	3 AAY75933	Aay75933 Neisseria
42	2294	98.0	441	3 AAY75912	Aay75912 Neisseria
43	2293	98.0	441	3 AAY75908	Aay75908 Neisseria
44	2293	98.0	441	3 AAY75922	Aay75922 Neisseria
45	2290.5	97.9	440	3 AAY75938	Aay75938 Neisseria

ALIGNMENTS

RESULT 1
AAB23783
ID AAB23783 standard; protein; 441 AA.
XX AAB23783;
AC
XX
DT 12-JAN-2001 (first entry)
XX
DE Neisseria MenB 919 protein sequence SEQ ID NO:31.
XX
XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
XX Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
XX bactericidal; antibacterial; vaccine; immunostimulatory; infection;
XX immune response.
XX
OS Neisseria meningitidis.
XX
PN WO200050075-A2.
PD
XX 31-AUG-2000.
XX
PF 09-FEB-2000; 2000MO-IB000176.
XX
PR 26-FEB-1999; 99US-0121792P.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;
XX
XX MPI; 2001-015529/02.
DR N-PSDB; AAA92388.
XX
PT Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
XX
PS Claim 5; Page 24; 39pp; English.
XX
The present invention describes an immunogenic composition (i) comprising
CC an oligonucleotide comprising at least 1 CG motif. Also described is an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (ii) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (i) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament

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OM protein - protein search, using SW model

Run on: April 18, 2005, 10:28:55 ; Search time 133 Seconds

(without alignments)
1102.071 Million cell updates/sec

Title: US-09-914-454b-31

Perfect score: 2340
Sequence: 1 MKXYLFRAALYGIAMAILAA.....KTTGYVWQLPVGKMEYRP 441

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.dep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.dep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.dep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.dep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.dep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.dep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.dep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.dep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.dep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.dep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.dep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.dep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.dep.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.dep.*
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.dep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.dep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2330	99.6	441	US-10-181-660-14	Sequence 14, Appli
2	2330	99.6	441	US-10-220-481-1	Sequence 1, Appli
3	2302	98.4	441	US-10-121-456A-1	Sequence 1, Appli
4	2262	96.7	440	US-10-220-481-3	Sequence 3, Appli
5	2236	95.6	832	US-10-220-480-4	Sequence 4, Appli
6	2236	95.6	832	US-10-220-481-89	Sequence 89, Appli
7	2236	95.6	897	US-10-220-480-10	Sequence 10, Appli
8	2236	95.6	897	US-10-220-481-95	Sequence 95, Appli
9	2227	95.2	420	US-10-220-481-2	Sequence 2, Appli
10	1015	43.4	194	US-10-220-481-8	Sequence 8, Appli
11	316.5	13.5	367	US-10-415-017-2	Sequence 2, Appli
12	316.5	13.5	367	US-10-415-017-6	Sequence 6, Appli
13	316.5	13.5	367	US-10-415-017-10	Sequence 10, Appli

14	315.5	13.5	367	US-10-415-017-8	Sequence 8, Appli
15	314.5	13.4	367	US-10-415-017-4	Sequence 4, Appli
16	238.5	10.2	196	US-10-220-481-9	Sequence 9, Appli
17	111	4.7	440	US-10-424-599-206691	Sequence 206691, A
18	108	4.6	676	US-10-282-122A-56343	Sequence 56343, A
19	106	4.5	1006	US-10-484-218-22	Sequence 22, Appli
20	102.5	4.4	503	US-10-369-493-17897	Sequence 17897, A
21	102	4.4	463	US-10-282-122A-52178	Sequence 52178, A
22	102	4.4	627	US-10-282-122A-55128	Sequence 55128, A
23	102	4.4	3745	US-10-205-032-14	Sequence 14, Appli
24	101.5	4.3	457	US-10-156-761-12009	Sequence 12009, A
25	101	4.3	359	US-10-016-668-4	Sequence 4, Appli
26	100	4.3	502	US-10-369-493-10113	Sequence 10113, A
27	100	4.3	506	US-10-282-122A-54065	Sequence 54065, A
28	98.5	4.2	357	US-10-424-599-253747	Sequence 253747, A
29	98.5	4.2	1616	US-09-712-363-262	Sequence 262, App
30	98.5	4.2	1616	US-10-282-122A-64807	Sequence 64807, A
31	98.5	4.2	1799	US-10-282-122A-62790	Sequence 62790, A
32	97.5	4.2	820	US-10-282-122A-66183	Sequence 66183, A
33	97.5	4.2	1279	US-10-332-288-6	Sequence 288, A
34	97	4.1	249	US-10-220-481-116	Sequence 116, App
35	97	4.1	2448	US-10-210-172-48	Sequence 48, Appli
36	97	4.1	3217	US-10-311-623-8	Sequence 8, Appli
37	97	4.1	3298	US-10-160-758-16	Sequence 16, Appli
38	97	4.1	3298	US-10-174-677-8	Sequence 8, Appli
39	97	4.1	3298	US-10-120-801-51	Sequence 51, Appli
40	97	4.1	3298	US-10-210-172-50	Sequence 15, Appli
41	97	4.1	4999	US-09-976-059-15	Sequence 107652, A
42	96.5	4.1	444	US-10-437-963-107662	Sequence 44, Appli
43	96.5	4.1	1446	US-10-166-087-44	Sequence 7994, Ap
44	95.5	4.1	882	US-10-369-493-7994	Sequence 54173, A
45	95	4.1	480	US-10-425-114-54173	

ALIGNMENTS

RESULT 1
US-10-181-660-14
; Sequence 14, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785NO
; CURRENT APPLICATION NUMBER: US/10/181,660
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqman9, version 1.02
; SEQ ID NO 14
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-14

Query Match 99.6%; Score 2330; DB 14; Length 441;
Best Local Similarity 99.5%; Pred. No. 1.4e-214;
Matches 439; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKXYLFRAALYGIAMAILAACOSKSIQTPPOPTSVINGBRPGVIGIPDAGTGGGAV 60
DB 1 MKXYLFRAALYGIAMAILAACOSKSIQTPPOPTSVINGBRPGVIGIPDAGTGGGAV 60
QY YTVVPHLSLPHMAAOEFASLQSPRIGCANLNKROSMOVCAQAPOTPVHSPAKOFFER 120
DB YTVVPHLSLPHMAAOEFASLQSPRIGCANLNKROSMOVCAQAPOTPVHSPAKOFFER 120
QY YTFWVAAGNSLACTVGTGYEVLKGDRTQAARFPIYIGIPDDFISVPLDAGLSGRA 180
DB YTFWVAAGNSLACTVGTGYEVLKGDRTQAARFPIYIGIPDDFISVPLDAGLSGRA 180

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OM protein - protein search, using sw model

Run on: April 18, 2005, 10:15:39 / Search time 46 Seconds
(without alignments)
922.426 Million cell updates/sec

Title: US-09-914-454b-31

Perfect score: 2340
Sequence: 1 MKKYLFRALYGIAMAILAA.....KTTGYWOLLPGMKPEYR 441

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR_79:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2333	99.7	441	2	membrane-bound lylt
2	2302	98.4	441	2	probable membrane-
3	611.5	26.1	385	2	probable membrane-
4	444	19.0	369	2	membrane-bound lylt
5	427.5	18.3	370	2	membrane-bound lylt
6	427.5	18.3	370	2	outer membrane lip
7	409.5	17.5	395	2	transglycosylase,
8	357	15.3	397	2	hypothetical prote
9	339	14.5	383	2	hypothetical prote
10	333.5	14.3	365	2	membrane-bound lylt
11	333.5	14.3	365	2	membrane-bound lylt
12	333.5	14.3	365	2	membrane-bound lylt
13	330.5	14.1	360	2	membrane-bound lylt
14	321	13.7	410	2	membrane-bound lylt
15	320.5	13.7	365	2	membrane-bound lylt
16	307.5	13.1	368	2	membrane-bound lylt
17	238.5	10.2	359	2	hypothetical prote
18	107.5	4.6	1094	2	probable recb prot
19	106.5	4.6	554	2	phosphoglycerate d
20	104	4.4	758	2	subtilisin-like pr
21	103	4.4	1301	2	alpha-amyase - Al
22	102	4.4	627	2	signal peptidase,
23	101.5	4.3	1528	2	hypothetical prote
24	101.5	4.3	1571	2	hypothetical prote
25	99.5	4.3	467	2	aminopeptidase, pr
26	99	4.2	3972	2	hypothetical prote
27	98.5	4.2	748	2	phosphoenolpyruvat
28	98.5	4.2	1616	2	polycetide synthas
29	98	4.2	484	2	xylokinase limpo

30	98	4.2	484	2	C91184	xylokinase limpo
31	98	4.2	1161	2	D83076	type 4 fibrinolytic
32	97.5	4.2	382	2	541941	beta-lactamase, cl
33	97.5	4.2	403	2	G75287	NADH oxidase-relat
34	97.5	4.2	820	2	D83337	probable TonB-depe
35	96	4.1	687	2	E87275	tonB-dependent rec
36	96	4.1	1161	2	E87275	plvii protein - Ps
37	95.5	4.1	692	2	T21722	hypothetical prote
38	95.5	4.1	3414	1	GNWVNE	hypothetical prote
39	95	4.1	484	1	KIECXV	genome polyprotein
40	94.5	4.0	548	1	S23437	xylokinase (EC 2
41	94.5	4.0	551	2	G84301	photinus-luciferin
42	94.5	4.0	1569	2	A65044	hypothetical prote
43	94	4.0	504	2	A61766	hypothetical prote
44	94	4.0	560	2	F84341	H+-transporting AT
45	93.5	4.0	643	2	E70682	hypothetical prote
						probable gamma-glu

ALIGNMENTS

RESULT 1		C81244		membrane-bound lylt murein transglycosylase A, probable NMB0033 [imported] - Neis	
C:Species: Neisseria meningitidis		C:Date: 31-Mar-2000		#sequence_revision 31-Mar-2000 #text_change 09-Jul-2004	
C:Accession: C81244		R:Retcelin, H. Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen		Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty,	
Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.		Science 287, 1809-1815, 2000		A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, J	
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS1		A:Reference number: A81000, MUID:20175755, PMID:10710307		A:Accession: C81244	
A:Status: Preliminary		A:Molecule type: DNA		A:Residues: 1-441 <TEXT>	
A:Cross-references: UNIPROT:Q9UR38; GB:A8002364; GB:A8002098; NID:g7225269; PIDN:AJ		A:Experimental source: serogroup B, strain MCS8		C:Genetics:	
A:Gene: NMB0033		Query Match		99.7%; Score 2333; DB 2; Length 441;	
Best Local Similarity		99.8%; Pred. No. 1.3e-177;		Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1	MKKYLFRAALYGIAMAILAACQSKSIQTFPODTSVINGPDRPVGIDPDAGTTVGCGGAV	60		
DB	1	MKKYLFRAALYGIAMAILAACQSKSIQTFPODTSVINGPDRPVGIDPDAGTTVGCGGAV	60		
QY	61	YTVVPHSLPMAAODPAKSLQSFRLGCANLKNRQGVCAQAFQPVMSFOKQFFER	120		
DB	61	YTVVPHSLPMAAODPAKSLQSFRLGCANLKNRQGVCAQAFQPVMSFOKQFFER	120		
QY	121	YTFPWOVAGNGSLAGTYTGYEPEVLKDDDRRTAARPPVIGIPDPDFSVPLPAGLRSGKA	180		
DB	121	YTFPWOVAGNGSLAGTYTGYEPEVLKDDDRRTAARPPVIGIPDPDFSVPLPAGLRSGKA	180		
QY	181	LVRIROTKNGSGTIDNTGTHYADLSRPITARTTAIKGRFEGSRFLPYHTRQINGCAL	240		
DB	181	LVRIROTKNGSGTIDNTGTHYADLSRPITARTTAIKGRFEGSRFLPYHTRQINGCAL	240		
QY	241	DGKAPITGVADPEVLEFPMHIQSGRLKTPSGYIRIGVADKNRHPVSIGRVWADSGYL	300		
DB	241	DGKAPITGVADPEVLEFPMHIQSGRLKTPSGYIRIGVADKNRHPVSIGRVWADSGYL	300		
QY	301	KLGQTSNGIKSYMRQNPORLAETVLAQNPBSYIFRFELAGSSNDGPVAGLGTPLMGAYAGA	360		
DB	301	KLGQTSNGIKSYMRQNPORLAETVLAQNPBSYIFRFELAGSSNDGPVAGLGTPLMGAYAGA	360		
QY	361	VDHRYITLAPPLVVAIRNHPTRKALRLMAQVTSAGIDANAVDVYFMVGDEAGELAGK	420		

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OM protein - protein search, using sw model

Run on: April 18, 2005, 09:58:14 ; Search time 183 Seconds
(without alignments)
1234.027 Million cell updates/sec

Title: US-09-914-454B-31

Perfect score: 2340
Sequence: 1 MKKYLFRAALYGAIAAIIAA.....KTTGYVWQLLPNGMKPEYRP 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2333	99.7	441	2	07DDU3
2	2333	99.7	441	2	09JRB3
3	2330	99.6	441	2	09JRB8
4	2330	99.6	441	2	09JPR2
5	2326	99.4	441	2	09JPR5
6	2325	99.4	441	2	09JPR8
7	2324	99.4	441	2	09JPR6
8	2317	99.0	441	2	09JPR4
9	2311	98.8	441	2	09JPR3
10	2307	98.6	441	2	09JPR0
11	2306	98.5	441	2	09JPR6
12	2302	98.4	441	2	07BXX2
13	2302	98.4	441	2	09JRX7
14	2302	98.4	441	2	09JRX7
15	2297	98.2	441	2	09JRX7
16	2297	98.2	441	2	09JRX7
17	2295	98.1	441	2	09JRX7
18	2294	98.0	441	2	09JRX7
19	2293	98.0	441	2	09JRX7
20	2289	97.8	441	2	09JRX7
21	2257	96.5	441	2	09JRX7
22	2254	96.3	441	2	09JRX7
23	2251	96.2	441	2	09JRX7
24	891.5	38.1	441	2	09JRX7
25	722	30.9	440	2	081Z6
26	678	29.0	372	2	062DC2
27	678	29.0	372	2	063OH7
28	674	28.8	429	2	07VU60
29	674	28.8	429	2	07W394
30	674	28.8	429	2	07W394
31	627	26.8	392	2	08BD56

32	621	26.5	399	2	0886J9	0886J9 pseudomonas
33	615	26.3	380	2	08XVF5	08XVF5 ralestonia s
34	611.5	26.1	385	2	0914B6	0914B6 pseudomonas
35	556.5	23.8	483	2	09E295	09E295 zymomonas m
36	552.5	23.6	400	2	083CK4	083CK4 coxiella bu
37	552.5	22.3	342	2	08KXU5	08KXU5 uncultured
38	511.5	21.9	520	2	06ND05	06ND05 rhodopseudo
39	492	21.0	494	2	089WN5	089WN5 bradyrhizob
40	466	19.9	424	2	072DP2	072DP2 desulfocib
41	446	19.1	369	2	08FY16	08FY16 bruceella su
42	444	19.0	366	2	098DU5	098DU5 rhizobium l
43	444	19.0	369	2	08YE26	08YE26 bruceella me
44	435	18.6	372	2	09ZTE5	09ZTE5 rhizobium m
45	427.5	18.3	370	2	080UB9	080UB9 agrobacteri

ALIGNMENTS

RESULT 1	ID	Q7DDU3	PRELIMINARY;	PRT;	441 AA.
AC	Q7DDU3				
DT	05-JUL-2004 (TEMBLrel. 27, Created)				
DT	05-JUL-2004 (TEMBLrel. 27, Last sequence update)				
DE	Membrane-bound lytic murein transglycosylase A, putative.				
GN	Ordered locus names: NMB0033;				
OS	Neisseria meningitidis (serogroup B).				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
OC	Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=491;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MC58 / Serogroup B;				
RX	MEDLINE=2017575; PubMed=10710307; DOI=10.1126/science.287.5459.1809;				
RA	Tetzelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,				
RA	Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,				
RA	Dodson R.J., Nelson W.C., Gwinn M.L., Deboy R.T., Peterson J.D.,				
RA	Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,				
RA	Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,				
RA	Citron H., Clark E.B., Cotton M.D., Uetrich T.R., Khouli H.M.,				
RA	Olin H., Vamathavan U.J., Gill J., Scarlato V., Maignani V., Pizarra M.,				
RA	Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappelli R.,				
RA	Venter J.C.;				
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain				
RT	MC58."				
RL	Science 287:1809-1815 (2000).				
DR	EMBL: A8002362; AAF40504.1; ..				
DR	TIGR: NMB0033; ..				
DR	GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl ..; IEA.				
DR	InterPro: IPR010611; 3D.				
DR	InterPro: IPR005300; MLCA.				
DR	Pfam: PRO6725; 3D: 1.				
DR	Pfam: PRO3562; MLCA, 1.				
KW	Complete Proteome.				
SQ	SEQUENCE 441 AA; 48007 MW; 6F161C1B955C30F CRC64;				
Query Match	99.7%; Score 2333; DB 2; Length 441;				
Best Local Similarity	99.8%; Pred. No. 1.8e-169;				
Matches	440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1 MKKYLFRAALYGAIAAIIAACOSKSIQTFPPQDTSVINGPDRPVGIIPDAGTTVGCGGAV 60				
DB	1 MKKYLFRAALYGAIAAIIAACOSKSIQTFPPQDTSVINGPDRPVGIIPDAGTTVGCGGAV 60				
QY	61 YVVVPHLSLPHAAADPFASLOSFLGCAANLKNRGQMDVCAQARQTPVHSAQAKQFPR 120				
DB	61 YVVVPHLSLPHAAADPFASLOSFLGCAANLKNRGQMDVCAQARQTPVHSAQAKQFPR 120				
QY	121 YFTPQVANGSLAGTAVTGYYEPVLKGDRTAQAAPFIYIGIPDDFISVPLAGRSQA 180				
DB	121 YFTPQVANGSLAGTAVTGYYEPVLKGDRTAQAAPFIYIGIPDDFISVPLAGRSQA 180				